We claim:

1. A method for preparing a probe for use in a qualitative or quantitative hybridization assay which comprises constructing an oligonucleotide that is sufficiently complementary to hybridize to a region of rRNA selected to be unique to a non-viral organism or group of non-viral organisms sought to be detected, said region of rRNA being selected by comparing one or more variable region rRNA sequences of said non-viral organism or group of non-viral organisms with one or more variable region rRNA sequences from one or more non-viral organisms sought to be distinguished therefrom.

2. The method of claim 1 wherein said variable region rRNA sequences from non-viral organisms sought to be distinguished are from the known nearest related organism to said non-viral organism or group of non-viral organisms sought to be detected.

3. The method of claim 1 wherein said region of rRNA is selected to have at least about a one base sequence difference from a corresponding rRNA sequence of the known nearest related organism to said non-viral organism or group of non-viral organisms sought to be detected.

4. The method of claim 1 wherein said region of rRNA is selected to have at least about a 10% or greater base sequence difference from the corresponding rRNA sequence of the known nearest related organism to said non-viral organism or group of non-viral organisms sought to be detected.

5. The method of claim 1 wherein said region of rRNA is chosen from the group consisting of 5S, 16S, and 23S rRNA.

6. The method of claim 1 wherein said region of rRNA is chosen from the group consisting of 5.0S, 5.8S, 18S and 28S rRNA.

7. The method of claim 1 wherein said oligonucleotide is at least about 10 nucleotides in length.

8. The method of claim 1 wherein said oligonucleotide is at least about 15 nucleotides in length.

9. The method of claim 1 wherein said oligonucleotide is at least about 20 nucleotides in length.

10. The method of claim 1 wherein said oligonucleotide is at least about 30 nucleotides in length.

11. The method of claim 1 wherein said oligonucleotide is about 20 nucleotides to about 50 nucleotides in length.

12. The method of claim 1 wherein said oligonucleotide is about 30 nucleotides to about 50 nucleotides in length.

13. The method of claim 3 wherein said oligonucleotide is at least about 10 nucleotides in length.

14. The method of claim 3 wherein said oligonucleotide is at least about 15 nucleotides in length.

15. The method of claim 1 wherein said oligonucleotide is at least about 20 nucleotides in length.

16. The method of claim 3 wherein said oligonucleotide is at least about 30 nucleotides in length.

17. The method of claim 3 wherein said oligonucleotide is about 20 nucleotides to about 50 nucleotides in length.

18. The method of claim 3 wherein said

oligonucleotide is at about 30 nucleotides to about 50 nucleotides in length.

19. The method of claim 4 wherein said oligonucleotide is at least about 10 nucleotides in length.

20. The method of claim 4 wherein said oligonucleotide is at least about 15 nucleotides in length.

21. The method of claim 4 wherein said oligonucleotide is at least about 20 nucleotides in length.

22. The method of claim 4 wherein said oligonucleotide is at least about 30 nucleotides in length.

23. The method of claim 4 wherein said oligonucleotide is about 20 nucleotides to about 50 nucleotides in length.

24. The method of claim 4 wherein said oligonucleotide is about 30 nucleotides to about 50 nucleotides in length.

25. The method of claim 1 wherein said probe is at least about 75% complementary to said region of rRNA.

26. The method of claim 3 wherein said oligonucleotide is at least about 75% complementary to said region of rRNA.

27. The method of claim 4 wherein said oligonucleotide is at least about 75% complementary to said region of rRNA.

28. The method of claim 1 wherein said probe is perfectly complementary to said region of rRNA.

29. The method of claim 3 wherein said probe is perfectly complementary to said region of rRNA.

30. The method of claim 4 wherein said probe is

~~perfectly complementary to said region of rRNA.~~

31. A hybridization assay probe for a non-viral organism or organisms comprising an oligonucleotide of at least about 10 nucleotides in length wherein at least about 10 contiguous nucleotides are substantially complementary to at least one variable region of nucleic acid selected to be unique to said non-viral organism or organisms.

32. A hybridization assay probe for a non-viral organism or organisms comprising an oligonucleotide of at least about 10 nucleotides in length which is at least about 75% complementary to at least one variable region of nucleic acid selected to be unique to said non-viral organism or organisms.

33. The probe of claim 31 or 32 wherein said nucleic acid is 5S, 16S, or 23S rRNA.

34. The probe of claim 31 or 32 wherein said nucleic acid is 5.0S, 5.8S, 18S, or 28S rRNA.

35. The probe of claim 31 wherein said non-viral organism is Mycobacterium avium.

36. The probe of claim 35 wherein said oligonucleotide comprises the sequence ACCGCAAAAGCTTTCCACCAGAAGACATGCGTCTTGAG.

37. A nucleotide polymer capable of hybridizing to the probe of claim 36 or to the complement thereof.

38. A nucleic acid hybrid formed between an oligonucleotide comprising the sequence ACCGCAAAAGCTTTCCACCAGAAGACATGCGTCTTGAG and a nucleic acid sequence substantially complementary thereto.

39. A nucleotide polymer of the structure ACCGCAAAAGCTTTCCACCAGAAGACATGCGTCTTGAG and the complement

thereto.

40. A nucleotide polymer capable of hybridizing to RNA of the species Mycobacterium avium in the region corresponding to bases 185-225 of E. coli 16S rRNA.

41. A nucleic acid hybrid formed between a nucleotide polymer of claim 40 and a nucleic acid sequence substantially complementary thereto.

42. The probe of claim 31 wherein said non-viral organism is Mycobacterium intracellulare.

43. The probe of claim 42 wherein said oligonucleotide comprises the sequence

ACCGCAAAAGCTTTCCACCTAAAGACATGCGCCTAAAG.

44. A nucleotide polymer capable of hybridizing to the probe of claim 43 or to the complement thereof.

45. A nucleic acid hybrid formed between an oligonucleotide comprising the sequence

ACCGCAAAAGCTTTCCACCTAAAGACATGCGCCTAAAG

and a nucleic acid sequence substantially complementary thereto.

46. A nucleotide polymer of the structure ACCGCAAAAGCTTTCCACCTAAAGACATGCGCCTAAAG and the complement thereto.

47. A nucleotide polymer capable of hybridizing to the RNA of the species Mycobacterium intracellulare in the region corresponding to bases 185-225 of E. coli 16S rRNA.

48. A nucleic acid hybrid formed between a nucleotide polymer of claim 47 and a nucleic acid sequence substantially complementary thereto.

49. The probe of claim 31 wherein said non-viral organisms are the Mycobacterium tuberculosis-complex bacteria.

50. The probe of claim 49 wherein said oligonucleotide comprises the sequence TAAAGCGCTTTCCACCACAAGACATGCATCCCGTG.

51. The probe of claim 49 wherein said oligonucleotide comprises the sequence TGCCCTACCCACACCCACCACAAGGTGATGT.

52. The probe of claim 49 wherein said oligonucleotide comprises the sequence CCATCACCACCCTCCTCCGGAGAGGAAAAGG.

53. The probe of claim 49 wherein said oligonucleotide comprises the sequence CTGTCCCTAAACCCGATTCAGGGTTCGAGGTTAGATGC.

54. The probe of claim 49 wherein said oligonucleotide comprise the sequence AGGCACTGTCCCTAAACCCGATT CAGGGTTC.

55. The probe of claim 49 wherein said oligonucleotide comprises the sequence CCGCTAAAGCGCTTTCCACCACAAGACATGCATCCCG.

56. The probe of claim 49 wherein said oligonucleotide comprise the sequence ACACCGCTAAAGCGCTTTCCACCACAAGACATGCATC.

57. A nucleotide polymer capable of hybridizing to the probe of claims 50 or 51 or 52 or 53 or 54 or 55 or 56 or to the complements thereof.

58. A nucleic acid hybrid formed between an oligonucleotide comprising a member of the group consisting of oligonucleotides of the sequences

TAAAGCGCTTTCCACCACAAGACATGCATCCCGTG,

TGCCCTACCCACACCCACCACAAGGTGATGT,

CCATCACCACCCTCCTCCGGAGAGGAAAAGG,

CTGTCCCTAAACCCGATTCAGGGTTCGAGGTTAGATGC,

AGGCACTGTCCCTAAACCCGATTCAGGGTTC,

CCGCTAAAGCGCTTTCCACCACAAGACATGCATCCCG, and

ACACCGCTAAAGCGCTTTCCACCACAAGACATGCATC;

and a nucleic acid sequence substantially complementary thereto.

59. A nucleotide polymer comprising a member of the group consisting of nucleotide polymers of the structures

TAAAGCGCTTTCCACCACAAGACATGCATCCCGTG,

TGCCCTACCCACACCCACCACAAGGTGATGT,

CCATCACCACCCTCCTCCGGAGAGGAAAAGG,

CTGTCCCTAAACCCGATTCAGGGTTCGAGGTTAGATGC,

AGGCACTGTCCCTAAACCCGATTCAGGGTTC,

CCGCTAAAGCGCTTTCCACCACAAGACATGCATCCCG, and

ACACCGCTAAAGCGCTTTCCACCACAAGACATGCATC;

and the complements thereto.

60. A nucleotide polymer capable of hybridizing to the rRNA of the species included in the Mycobacterium tuberculosis complex in the region corresponding to bases 185-225 of E. coli 16S rRNA.

61. A nucleic acid hybrid formed between a nucleotide polymer of claim 60 and a nucleic acid substantially complementary thereto.

62. A nucleotide polymer capable of hybridizing to the RNA of the species included in the Mycobacterium tuberculosis complex in the region corresponding to bases 540-575 of E. coli 23S rRNA.

63. A nucleic acid hybrid formed between a nucleotide polymer of claim 62 and a nucleic acid substantially

complementary thereto.

64. A nucleotide polymer capable of hybridizing to the RNA of the species included in the Mycobacterium tuberculosis complex in the region corresponding to bases 1155-1190 of E. coli 23S rRNA.

65. A nucleic acid hybrid formed between a nucleotide polymer of claim 64 and a nucleic acid substantially complemen-tary thereto.

66. A nucleotide polymer capable of hybridizing to the RNA of the species included in the Mycobacterium tuberculosis complex in the region corresponding to bases 2195-2235 of E. coli 23S rRNA.

67. A nucleic acid hybrid formed between a nucleotide polymer of claim 66 and a nucleic acid substantially complemen-tary thereto.

68. The probe of claim 31 wherein said non-viral organisms are the genus Mycobacterium.

69. The probe of claim 68 wherein said oligonucleotide comprises the sequence CCA TGC ACC ACC TGC ACA CAG GCC ACA AGG.

70. The probe of claim 68 wherein said oligonucleotide comprises the sequence GGC TTG CCC CAG TAT TAC CAC TGA CTG GTA CGG.

71. The probe of claim 68 wherein said oligonucleotide comprises the sequence CAC CGA ATT CGC CTC AAC CGG CTA TGC GTC ACC TC.

72. The probe of claim 68 wherein said oligonucleotide comprises the sequence GGG GTA CGG CCC GTG TGT GTG CTC GCT AGA GGC.

73. A nucleotide polymer capable of hybridizing to the probes of claims 69 or 70 or 71 or 72 or to the complements thereof.

74. A nucleic acid hybrid formed between an oligonucleotide comprising a member of the group consisting of oligonucleotides of the sequence

CCA TGC ACC ACC TGC ACA CAG GCC ACA AGG,

GGC TTG CCC CAG TAT TAC CAC TGA CTG GTA CGG,

CAC CGA ATT CGC CTC AAC CGG CTA TGC GTC ACC TC,

and

GGG GTA CGG CCC GTG TGT GTG CTC GCT AGA GGC;

and a nucleic acid sequence substantially complementary thereto.

75. A nucleotide polymer comprising a member of the group consisting of nucleotide polymers of the structures

CCA TGC ACC ACC TGC ACA CAG GCC ACA AGG,

GGC TTG CCC CAG TAT TAC CAC TGA CTG GTA CGG,

CAC CGA ATT CGC CTC AAC CGG CTA TGC GTC ACC TC,

and

GGG GTA CGG CCC GTG TGT GTG CTC GCT AGA GGC;

and the complements thereto.

76. A nucleotide polymer capable of hybridizing to RNA of the genus Mycobacterium in the region corresponding to bases 1025-1060 of E. coli 16S rRNA.

77. A nucleic acid hybrid formed between a nucleotide polymer of claim 76 and a nucleic acid sequence substantially complementary thereto.

78. A nucleotide polymer capable of hybridizing to RNA of the genus Mycobacterium in the region corresponding to bases 1440-1475 of E. coli 23S rRNA.

79. A nucleic acid hybrid formed between a nucleotide polymer of claim 78 and a nucleic acid sequence substantially complementary thereto.

80. A nucleotide polymer capable of hybridizing to RNA of the genus Mycobacterium in the region corresponding to bases 1515-1555 of E. coli 23S rRNA.

81. A nucleic acid hybrid formed between a nucleotide polymer of claim 80 and a nucleic acid sequence substantially complementary thereto.

82. A nucleotide polymer capable of hybridizing to RNA of the genus Mycobacterium in the region corresponding to bases 1570-1610 of E. coli 23S rRNA.

83. A nucleic acid hybrid formed between a nucleotide polymer of claim 82 and a nucleic acid sequence substantially complementary thereto.

84. The probe of claim 31 wherein said non-viral organism is Mycoplasma pneumoniae.

85. The probe of claim 84 wherein said oligonucleotide comprises the sequence

GCTTGGTGCTTTCCTATTCTCACTGAAACAGCTACATTCGGC.

86. The probe of claim 84 wherein said oligonucleotide comprises the sequence

AATAACGAACCCTTGCAGGTCCTTTCAACTTTGAT.

87. The probe of claim 84 wherein said oligonucleotide comprises the sequence CAGTCAAACTCTAGCCATTACCT GCTAAAGTCATT.

88. The probe of claim 84 wherein said oligonucleotide comprise the sequence

TACCGAGGGGATCGCCCCGACAGCTAGTAT.

89. The probe of claim 84 wherein said oligonucleotide comprises the sequence CTTTACAGATTTGCTCACTTTTACAAGCTGGCGAC.

90. A nucleotide polymer capable of hybridizing to the probes of claims 85 or 86 or 87 or 88 or 89 or to the complements thereof.

91. A nucleic acid hybrid formed between an oligonucleotide comprising a member of the group consisting of oligonucleotides of the sequence

GCTTGGTGCTTTCCTATTCTCACTGAAACAGCTACATTCGGC,

AATAACGAACCCTTGCAGGTCCTTTCAACTTTGAT,

CAGTCAAACTCTAGCCATTACCTGCTAAAGTCATT,

TACCGAGGGGATCGCCCCGACAGCTAGTAT, and

CTTTACAGATTTGCTCACTTTTACAAGCTGGCGAC;

and a nucleic acid sequence substantially complementary thereto.

92. A nucleotide polymer comprising a member of the group consisting of nucleotide polymers of the structures

GCTTGGTGCTTTCCTATTCTCACTGAAACAGCTACATTCGGC,

AATAACGAACCCTTGCAGGTCCTTTCAACTTTGAT,

CAGTCAAACTCTAGCCATTACCTGCTAAAGTCATT,

TACCGAGGGGATCGCCCCGACAGCTAGTAT, and

CTTTACAGATTTGCTCACTTTTACAAGCTGGCGAC;

and the complements thereto.

93. A nucleotide polymer capable of hybridizing to the RNA of the species Mycoplasma pneumoniae in the region corresponding to bases 190-230 of E. coli 16S rRNA.

94. A nucleic acid hybrid formed between a nucleotide polymer of claim 93 and a nucleic acid sequence substantially complementary thereto.

95. A nucleotide polymer capable of hybridizing to the RNA of the species Mycoplasma pneumoniae in the region corresponding to bases 450-490 of E. coli 16S rRNA.

96. A nucleic acid hybrid formed between a nucleotide polymer of claim 95 and a nucleic acid sequence substantially complementary thereto.

97. A nucleotide polymer capable of hybridizing to the RNA of the species Mycoplasma pneumoniae in the region corresponding to bases 820-860 of E. coli 16S rRNA.

98. A nucleic acid hybrid formed between a nucleotide polymer of claim 97 and a nucleic acid sequence substantially complementary thereto.

99. A nucleotide polymer capable of hybridizing to the RNA of the species Mycoplasma pneumoniae in the region corresponding to bases 1255-1290 of E. coli 16S rRNA.

100. A nucleic acid hybrid formed between a nucleotide polymer of claim 99 and a nucleic acid sequence substantially complementary thereto.

101. A nucleotide polymer capable of hybridizing to the RNA of the species Mycoplasma pneumoniae in the region corresponding to bases 65-120 of E. coli 5S rRNA.

102. A nucleic acid hybrid formed between a nucleotide polymer of claim 101 and a nucleic acid sequence substantially complementary thereto.

103. The probe of claim 31 wherein said non-viral organisms are the genus Legionella.

104. The probe of claim 103 wherein said oligonucleotide comprises the sequence TACCCTCTCCCATACTCGAGT CAACCAGTATTATCTGACC.

105. The probe of claim 103 wherein said oligonucleotide comprises the sequence GGATTTCACGTGTCCCGGCCTACTT GTTCGGGTGCGTAGTTC.

106. The probe of claim 103 wherein said oligonucleotide comprises the sequence CATCTCTGCAAAATTCACTGTAT GTCAAGGGTAGGTAAGG.

107. The probe of claim 103 wherein said oligonucleotide comprises the sequence GCGGTACGGTTCTCTATAA GTTATGGCTAGC.

108. The probe of claim 103 wherein said oligonucleotide comprises the sequence GTACCGAGGGTACCTTTGTGCT.

109. The probe of claim 103 wherein said oligonucleotide comprises the sequence CACTCTTGGTACGATGTCCGAC.

110. A nucleotide polymer capable of hybridizing to the probes of claims 104 or 105 or 106 or 107 or 108 or 109 or to the complements thereof.

111. A nucleic acid hybrid formed between an oligonucleotide comprising a member of the group consisting of oligonucleotides of the sequences

TACCCTCTCCCATACTCGAGTCAACCAGTATTATCTGACC,

GGATTTCACGTGTCCCGGCCTACTTGTTCGGGTGCGTAGTTC,

CATCTCTGCAAAATTCACTGTATGTCAAGGGTAGGTAAGG,

GCGGTACGGTTCTCTATAAGTTATGGCTAGC,

GTACCGAGGGTACCTTTGTGCT, and

CACTCTTGGTACGATGTCCGAC;

and a nucleic acid sequence substantially complementary thereto.

112. A nucleotide polymer comprising a member of the group consisting of nucleotide polymers of the structures

TACCCTCTCCCATACTCGAGTCAACCAGTATTATCTGACC,

GGATTTCACGTGTCCCGGCCTACTTGTTCGGGTGCGTAGTTC,

CATCTCTGCAAAATTCACTGTATGTCAAGGGTAGGTAAGG,

GCGGTACGGTTCTCTATAAGTTATGGCTAGC,

GTACCGAGGGTACCTTTGTGCT, and

CACTCTTGGTACGATGTCCGAC;

and the complements thereto.

113. A nucleotide polymer capable of hybridizing to the RNA of the genus Legionella in the region corresponding to bases 630-675 of E. coli 16S rRNA.

114. A nucleic acid hybrid formed between a nucleotide polymer of claim 113 and a nucleic acid sequence substantially complementary thereto.

115. A nucleotide polymer capable of hybridizing to the RNA of the genus Legionella in the region corresponding to bases 975-1020 of E. coli 16S rRNA.

116. A nucleic acid hybrid formed between a nucleotide polymer of claim 115 and a nucleic acid sequence substantially complementary thereto.

117. A nucleotide polymer capable of hybridizing to the RNA of the genus Legionella in the region corresponding to bases 350-395 of E. coli 23S rRNA.

118. A nucleic acid hybrid formed between a nucleotide polymer of claim 117 and a nucleic acid sequence substantially complementary thereto.

119. A nucleotide polymer capable of hybridizing to the RNA of the genus Legionella in the region corresponding to bases 1585-1620 of E. coli 23S rRNA.

120. A nucleic acid hybrid formed between a nucleotide polymer of claim 119 and a nucleic acid sequence

substantially complementary thereto.

121. A nucleotide polymer capable of hybridizing to the RNA of the genus Legionella in the region corresponding to bases 2280-2330 of E. coli 23S rRNA.

122. A nucleic acid hybrid formed between a nucleotide polymer of claim 121 and a nucleic acid sequence substantially complementary thereto.

123. The probe of claim 31 wherein said non-viral organism is Chlamydia trachomatis.

124. The probe of claim 123 wherein said oligonucleotide comprises the sequence CCGACTCGGGGTTGAGCCCATCTTTGACAA.

125. The probe of claim 123 wherein said oligonucleotide comprise the sequence TTACGTCCGACACGGATGGGGTTGAGACCATC.

126. The probe of claim 123 wherein said oligonucleotide comprises the sequence CCGCCACTAAACAATCGTCGAAACAATTGCTCCGTTCGA.

127. The probe of claim 123 wherein said oligonucleotide comprises the sequence CGTTACTCGGATGCCCAAATATCGCCACATTCG.

128. The probe of claim 123 wherein said oligonucleotide comprises the sequence CATCCATCTTTCCAGATGTGTTCAACTAGGAGTCCTGATCC.

129. The probe of claim 123 wherein said oligonucleotide comprises the sequence GAGGTCGGTCTTTCTCTCCTTTCGTCTACG.

130. The probe of claim 123 wherein said oligonucleotide comprises the sequence

CCGTTCTCATCGCTCTACGGACTCTTCCAATCG.

131. The probe of claim 123 wherein said oligonucleotide comprises the sequence CGAAGATTCCCCTTGATCGCGACCTGATCT.

132. The probe of claim 123 wherein said oligonucleotide comprises the sequence CCGGGGCTCCTATCGTTCCATAGTCACCCTAAAAG.

133. The probe of claim 123 wherein said oligonucleotide comprises the sequence TACCGCGTGTCTTATCGACACACCCGCG.

134. A nucleotide polymer capable of hybridizing to the probes of claims 124 or 125 or 126 or 127 or 128 or 129 or 130 or 131 or 132 or 133 or to the complements thereof.

135. A nucleic acid hybrid formed between an oligonucleotide comprising a member of the group consisting of oligonucleotides of the sequence

CCGACTCGGGGTTGAGCCCATCTTTGACAA,

TTACGTCCGACACGGATGGGGTTGAGACCATC,

CCGCCACTAAACAATCGTCGAAACAATTGCTCCGTTCGA,

CGTTACTCGGATGCCCAAATATCGCCACATTCG,

CATCCATCTTTCCAGATGTGTTCAACTAGGAGTCCTGATCC,

GAGGTCGGTCTTTCTCTCCTTTCGTCTACG,

CCGTTCTCATCGCTCTACGGACTCTTCCAATCG,

CGAAGATTCCCCTTGATCGCGACCTGATCT,

CCGGGGCTCCTATCGTTCCATAGTCACCCTAAAAG, and

TACCGCGTGTCTTATCGACACACCCGCG;

and a nucleic acid sequence substantially complementary thereto.

136. A nucleotide polymer comprising a member of the group consisting of nucleotide polymers of the structures

CCGACTCGGGGTTGAGCCCATCTTTGACAA,

TTACGTCCGACACGGATGGGGTTGAGACCATC,

CCGCCACTAAACAATCGTCGAAACAATTGCTCCGTTCGA,

CGTTACTCGGATGCCCAAATATCGCCACATTCG,

CATCCATCTTTCCAGATGTGTTCAACTAGGAGTCCTGATCC,

GAGGTCGGTCTTTCTCTCCTTTCGTCTACG,

CCGTTCTCATCGCTCTACGGACTCTTCCAATCG,

CGAAGATTCCCCTTGATCGCGACCTGATCT,

CCGGGGCTCCTATCGTTCCATAGTCACCCTAAAAG, and

TACCGCGTGTCTTATCGACACACCCGCG;

and the complements thereto.

137. A nucleotide polymer capable of hybridizing to the RNA of the species Chlamydia trachomatis in the region corresponding to bases 60-105 of E. coli 16S rRNA.

138. A nucleic acid hybrid formed between a nucleotide polymer of claim 137 and a nucleic acid substantially complemen-tary thereto.

139. A nucleotide polymer capable of hybridizing to the RNA of the species Chlamydia trachomatis in the region corresponding to bases 175-210 of E. coli 16S rRNA.

140. A nucleic acid hybrid formed between a nucleotide polymer of claim 139 and a nucleic acid substantially complementary thereto.

141. A nucleotide polymer capable of hybridizing to the RNA of the species Chlamydia trachomatis in the region corresponding to bases 600-635 of E. coli 16S rRNA.

142. A nucleic acid hybrid formed between a nucleotide polymer of claim 141 and a nucleic acid substantially complemen-tary thereto.

143. A nucleotide polymer capable of hybridizing to the RNA of the species Chlamydia trachomatis in the region corresponding to bases 830-870 of E. coli 16S rRNA.

144. A nucleic acid hybrid formed between a nucleotide polymer of claim 143 and a nucleic acid substantially complemen-tary thereto.

145. A nucleotide polymer capable of hybridizing to the RNA of the species Chlamydia trachomatis in the region corresponding to bases 275-320 of E. coli 23S rRNA.

146. A nucleic acid hybrid formed between a nucleotide polymer of claim 145 and a nucleic acid substantially complemen-tary thereto.

147. A nucleotide polymer capable of hybridizing to the RNA of the species Chlamydia trachomatis in the region corresponding to bases 330-365 of E. coli 23S rRNA.

148. A nucleic acid hybrid formed between a nucleotide polymer of claim 147 and a nucleic acid substantially complemen-tary thereto.

149. A nucleotide polymer capable of hybridizing to the RNA of the species Chlamydia trachomatis in the region corresponding to bases 1160-1190 of E. coli 23S rRNA.

150. A nucleic acid hybrid formed between a nucleotide polymer of claim 149 and a nucleic acid substantially complemen-tary thereto.

151. A nucleotide polymer capable of hybridizing to the RNA of the species Chlamydia trachomatis in the region corresponding to bases 1450-1490 of E. coli 23S rRNA.

152. A nucleic acid hybrid formed between a nucleotide polymer of claim 151 and a nucleic acid substantially

complemen-tary thereto.

153. A nucleotide polymer capable of hybridizing to the RNA of the species Chlamydia trachomatis in the region corresponding to bases 1510-1545 of E. coli 23S rRNA.

154. A nucleic acid hybrid formed between a nucleotide polymer of claim 153 and a nucleic acid substantially complemen-tary thereto.

155. A nucleotide polymer capable of hybridizing to the RNA of the species Chlamydia trachomatis in the region corresponding to bases 1710-1750 of E. coli 23S rRNA.

156. A nucleic acid hybrid formed between a nucleotide polymer of claim 155 and a nucleic acid substantially complementary thereto.

157. The probe of claim 31 wherein said non-viral organism is Campylobacter.

158. The probe of claim 157 wherein said oligonucleotide comprises the sequence

CGC TCC GAA AAG TGT CAT CCT CC.

159. The probe of claim 157 wherein said oligonucleotide comprises the sequence

CCT TAG GTA CCG TCA GAA TTC TTC CC.

160. The probe of claim 157 wherein said oligonucleotide comprises the sequence

GCC TTC GCA ATG GGT ATT CTT GGTG.

161. The probe of claim 157 wherein said oligonucleotide comprises the sequence

GGT TCT TAG GAT ATC AAG CCC AGG.

162. A nucleotide polymer capable of hybridizing to the probes of claims 158 or 159 or 160 or 161 or to the

complements thereof.

163. A nucleic acid hybrid formed between an oligonucleotide comprising a member of the group consisting of oligonucleotides of the sequence

CGC TCC GAA AAG TGT CAT CCT CC,

CCT TAG GTA CCG TCA GAA TTC TTC CC,

GCCTTCGCAATGGGTATTCTTGGTG, and

GGT TCT TAG GAT ATC AAG CCC AGG;

and a nucleic acid sequence substantially complementary thereto.

164. A nucleotide polymer comprising a member of the group consisting of nucleotide polymers of the structures

CGC TCC GAA AAG TGT CAT CCT CC,

CCT TAG GTA CCG TCA GAA TTC TTC CC,

GCCTTCGCAATGGGTATTCTTGGTG, and

GGT TCT TAG GAT ATC AAG CCC AGG;

and the complements thereto.

165. A nucleotide polymer capable of hybridizing to the RNA of the genus Campylobacter in the region corresponding to bases 405-428 of E. coli 16S rRNA.

166. A nucleic acid hybrid formed between a nucleotide polymer of claim 165 and a nucleic acid substantially complemen-tary thereto.

167. A nucleotide polymer capable of hybridizing to the RNA of the genus Campylobacter in the region corresponding to bases 440-475 of E. coli 16S rRNA.

168. A nucleic acid hybrid formed between a nucleotide polymer of claim 167 and a nucleic acid substantially complemen-tary thereto.

169. A nucleotide polymer capable of hybridizing

to the RNA of the genus Campylobacter in the region corresponding to bases 705-735 of E. coli 16S rRNA.

170. A nucleic acid hybrid formed between a nucleotide polymer of claim 169 and a nucleic acid substantially complemen-tary thereto.

171. A nucleotide polymer capable of hybridizing to the RNA of the genus Campylobacter in the region corresponding to bases 980-1010 of E. coli 16S rRNA.

172. A nucleic acid hybrid formed between a nucleotide polymer of claim 171 and a nucleic acid sequence substantially complemantary thereto.

173. The probe of claim 31 wherein said non-viral organisms are the sub-generic group of Streptococci known as enterococci.

174. The probe of claim 173 wherein said oligonucleotide comprises the sequence TGC AGC ACT GAA GGG CGG AAA CCC TCC AAC ACT TA.

175. A nucleotide polymer capable of hybridizing to the probe of claim 174 or to the complement thereof.

176. A nucleic acid hybrid formed between an oligonucleotide comprising the sequence

TGC AGC ACT GAA GGG CGG AAA CCC TCC AAC ACT TA

and a nucleic acid sequence substantially complementary thereto.

177. A nucleotide polymer of the structure

TGC AGC ACT GAA GGG CGG AAA CCC TCC AAC ACT TA

and the complement thereto.

178. A nucleotide polymer capable of hybridizing to the RNA of the sub-generic group Streptococci known as enterococci in the region corresponding to bases 825-860 of E.

coli 16S rRNA.

179. A nucleic acid hybrid formed between a nucleotide polymer of claim 178 and a nucleic acid sequence substantially complementary thereto.

180. The probe of claim 31 wherein said non-viral organisms are the subgeneric grouping known as Group I Pseudomonas.

181. The probe of claim 180 wherein said oligonucleotide comprises the sequence

CAG ACA AAG TTT CTC GTG CTC CGT CCT ACT CGA TT.

182. A nucleotide polymer capable of hybridizing to the probe of claim 181 or to the complement thereof.

183. A nucleic acid hybrid formed between an oligonucleotide comprising the sequence

CAG ACA AAG TTT CTC GTG CTC CGT CCT ACT CGA TT

and a nucleic acid substantially complementary thereto.

184. A nucleotide polymer of the structure

CAG ACA AAG TTT CTC GTG CTC CGT CCT ACT CGA TT

and the complement thereto.

185. A nucleotide polymer capable of hybridizing to the RNA of the sub-generic grouping known as group I Pseudomonas in the region corresponding to the bases 365-405 of E. coli 23S rRNA.

186. A nucleic acid hybrid formed between a nucleotide polymer of claim 185 and a nucleic acid sequence substantially complementary thereto.

187. The probe of claim 31 wherein said non-viral organism is Enterobacter cloacae.

188. The probe of claim 187 wherein said

oligonucleotide comprises the sequence

GTG TGT TTT CGT GTA CGG GAC TTT CAC CC.

189. A nucleotide polymer capable of hybridizing to the probe of claim 189 or to the complement thereof.

190. A nucleic acid hybrid formed between an oligonucleotide comprising a member of the group consisting of oligonucleotides of the sequence

GTG TGT TTT CGT GTA CGG GAC TTT CAC CC

and a nucleic acid sequence substantially complementary thereto.

191. A nucleotide polymer of the structure

GTG TGT TTT CGT GTA CGG GAC TTT CAC CC

and the complement thereto.

192. A nucleotide polymer capable of hybridizing to the RNA of the species Enterobacter cloacae in the region corresponding to bases 305-340 of E. coli 23S rRNA.

193. A nucleic acid hybrid formed between a nucleotide polymer of claim 192 and a nucleic acid sequence substantially complementary thereto.

194. The probe of claim 31 wherein said non-viral organism is Proteus mirabilis.

195. The probe of claim 194 wherein said oligonucleotide comprises the sequence

CCG TTC TCC TGA CAC TGC TAT TGA TTA AGA CTC.

196. A nucleotide polymer capable of hybridizing to the probe of claim 195 or to the complement thereof.

197. A nucleic acid hybrid formed between an oligonucleotide comprising the sequence

CCG TTC TCC TGA CAC TGC TAT TGA TTA AGA CTC

and a nucleic acid sequence substantially complementary thereto.

198. A nucleotide polymer of the structure

CCG TTC TCC TGA CAC TGC TAT TGA TTA AGA CTC

and the complement thereto.

199. A nucleotide polymer capable of hybridizing to the RNA of the species Proteus mirabilis in the region corresponding to bases 270-305 of E. coli 23S rRNA.

200. A nucleic acid hybrid formed between a nucleotide polymer of claim 199 and a nucleic acid sequence substantially complementary thereto.

201. The probe of claim 31 wherein said non-viral organisms are the genus Salmonella.

202. The probe of claim 201 wherein said oligonucleotide comprises the sequence CTC CTT TGA GTT CCC GAC CTA ATC GCT GGC.

203. The probe of claim 201 wherein said oligonucleotide comprises the sequence CTC ATC GAG CTC ACA GCA CAT GCG CTT TTG TGT A.

204. A nucleotide polymer capable of hybridizing to the probe of claim 202 or 203 or to the complement thereof.

205. A nucleic acid hybrid formed between an oligonucleotide comprising a member of the group consisting of oligonucleotides of the sequence

CTC CTT TGA GTT CCC GAC CTA ATC GCT GGC and

CTC ATC GAG CTC ACA GCA CAT GCG CTT TTG TGT A;

and a nucleic acid sequence substantially complementary thereto.

206. A nucleotide polymer comprising a member of the group consisting of nucleotide polymers of the structures

CTC CTT TGA GTT CCC GAC CTA ATC GCT GGC and

CTC ATC GAG CTC ACA GCA CAT GCG CTT TTG TGT A;

and the complements thereto.

207. A nucleotide polymer capable of hybridizing to the RNA of the genus Salmonella in the region corresponding to bases 1125-1155 of E. coli 16S rRNA.

208. A nucleic acid hybrid formed between a nucleotide polymer of claim 207 and a nucleic acid sequence substantially complementary thereto.

209. A nucleotide polymer capable of hybridizing to the RNA of the genus Salmonella in the region corresponding to bases 335-375 of E. coli 23S rRNA.

210. A nucleic acid hybrid formed between a nucleotide polymer of claim 209 and a nucleic acid sequence substantially complementary thereto.

211. The probe of claim 31 wherein said non-viral organism is Escherichia coli.

212. The probe of claim 211 wherein said oligonucleotide comprises the sequence

GCA CAT TCT CAT CTC TGA AAA CTT CCG TGG.

213. A nucleotide polymer capable of hybridizing to the probe of claim 212 or to the complement thereof.

214. A nucleic acid hybrid formed between an oligonucleotide comprising the sequence

GCA CAT TCT CAT CTC TGA AAA CTT CCG TGG

and a nucleic acid substantially complementary thereto.

215. A nucleotide polymerof the structure GCA CAT TCT CAT CTC TGA AAA CTT CCG TGG

and the complement thereto.

216. A nucleotide polymer capable of hybridizing to the RNA of the species Escherichia coli in the region

corresponding to bases 995-1030 of E. coli 16 sRNA.

217. A nucleic acid hybrid formed between a nucleotide polymer of claim 216 and a nucleic acid sequence substantially complementary thereto.

218. The probe of claim 31 wherein said non-viral organisms are the phylogenetic group bacteria.

219. The probe of claim 218 wherein said oligonucleotide comprises the sequence CCA CTG CTG CCT CCC GTA GGA GTC TGG GCC.

220. The probe of claim 218 wherein said oligonucleotide comprises the sequence CCA GAT CTC TAC GCA TTT CAC CGC TAC ACG TGG.

221. The probe of claim 218 wherein said oligonucleotide comprises the sequence GCT CGT TGC GGG ACT TAA CCC AAC AT.

222. The probe of claim 218 wherein said oligonucleotide comprises the sequence GGG GTT CTT TTC GCC TTT CCC TCA CGG.

223. The probe of claim 218 wherein said oligonucleotide comprises the sequence GGC TGC TTC TAA GCC AAC ATC CTG.

224. The probe of claim 218 wherein said oligonucleotide comprises the sequence GGA CCG TTA TAG TTA CGG CCG CC.

225. The probe of claim 218 wherein said oligonucleotide comprises the sequence GGT CGG AAC TTA CCC GAC AAG GAA TTT CGC TAC C.

226. A nucleotide polymer capable of hybridizing to the probes of claim 219 or 220 or 221 or 222 or 223 or 224 or

225 or to the complements thereof.

227. A nucleic acid hybrid formed between an oligonucleotide comprising a member of the group consisting of oligonucleotides of the sequences

CCA CTG CTG CCT CCC GTA GGA GTC TGG GCC,

CCA GAT CTC TAC GCA TTT CAC CGC TAC ACG TGG,

GCT CGT TGC GGG ACT TAA CCC AAC AT,

GGG GTT CTT TTC GCC TTT CCC TCA CGG,

GGC TGC TTC TAA GCC AAC ATC CTG,

GGA CCG TTA TAG TTA CGG CCG CC, and

GGT CGG AAC TTA CCC GAC AAG GAA TTT CGC TAC C;

and a nucleic acid sequence substantially similar thereto.

228. A nucleotide polymer comprising a member of the group consisting of nucleotide polymers of the structures

CCA CTG CTG CCT CCC GTA GGA GTC TGG GCC,

CCA GAT CTC TAC GCA TTT CAC CGC TAC ACG TGG,

GCT CGT TGC GGG ACT TAA CCC AAC AT,

GGG GTT CTT TTC GCC TTT CCC TCA CGG,

GGC TGC TTC TAA GCC AAC ATC CTG,

GGA CCG TTA TAG TTA CGG CCG CC, and

GGT CGG AAC TTA CCC GAC AAG GAA TTT CGC TAC C;

and the complements thereto.

229. A nucleotide polymer capable of hybridizing to the RNA of the phylogenetic group bacteria in the region corresponding to bases 330-365 of E. coli 16S rRNA.

230. A nucleic acid hybrid formed between a nucleotide polymer of claim 229 and a nucleic acid sequence substantially complementary thereto.

231. A nucleotide polymer capable of hybridizing

to the RNA of the phylogenetic group bacteria in the region corresponding to bases 675-715 of E. coli 16S rRNA.

232. A nucleic acid hybrid formed between a nucleotide polymer of claim 231 and a nucleic acid sequence substantially complementary thereto.

233. A nucleotide polymer capable of hybridizing to the RNA of the phylogenetic group bacteria in the region corresponding to bases 1080-1110 of E. coli 16S rRNA.

234. A nucleic acid hybrid formed between a nucleotide polymer of claim 233 and a nucleic acid sequence substantially complementary thereto.

235. A nucleotide polymer capable of hybridizing to the RNA of the phylogenetic group bacteria in the region corresponding to bases 460-490 of E. coli 23S rRNA.

236. A nucleic acid hybrid formed between a nucleotide polymer of claim 235 and a nucleic acid sequence substantially complementary thereto.

237. A nucleotide polymer capable of hybridizing to the RNA of the phylogenetic group bacteria in the region corresponding to bases 1050-1080 of E. coli 23S rRNA.

238. A nucleic acid hybrid formed between a nucleotide polymer of claim 237 and a nucleic acid sequence substantially complementary thereto.

239. A nucleotide polymer capable of hybridizing to the RNA of the phylogenetic group bacteria in the region corresponding to bases 1900-1960 of E. coli 23S rRNA.

240. A nucleic acid hybrid formed between a nucleotide polymer of claim 239 and a nucleic acid sequence substantially complementary thereto.

241. The probe of claim 31 wherein said non-viral organisms are fungi.

242. The probe of claim 241 wherein said oligonucleotide comprises the sequence

CCC GAC CGT CCC TAT TAA TCA TTA CGA TGG.

243. The probe of claim 241 wherein said oligonucleotide comprise the sequence CCCGACCGTCCCTATTAATCATTACGATGGTCCTAGAAAC.

244. The probe of claim 241 wherein said oligonucleotide comprises the sequence CCCGACCGTCCCTATTAATCATTACGATGG.

245. The probe of claim 241 wherein said oligonucleotide comprises the sequence

CGA CTT GGC ATG AAA ACT ATT CCT TCC TGT GG.

246. The probe of claim 241 wherein said oligonucleotide comprises the sequence

GCT CTT CAT TCA ATT GTC CAC GTT CAA TTA AGC AAC AAG G.

247. The probe of claim 241 wherein said oligonucleotide comprises the sequence

GCT CTG CAT TCA AAC GTC CGC GTT CAA TAA AGA AAC AGG G.

248. A nucleotide polymer capable of hybridizing to the probes of claims 242 or 243 or 244 or 245 or 246 or 247 or to the complements thereof.

249. A nucleic acid hybrid formed between an oligonucleotide comprising a member of the group consisting of oligonucleotides of the sequence

CCC GAC CGT CCC TAT TAA TCA TTA CGA TGG,

CCCGACCGTCCCTATTAATCATTACGATGGTCCTAGAAAC

CCCGACCGTCCCTATTAATCATTACGATGG

CGA CTT GGC ATG AAA ACT ATT CCT TCC TAT GG,

GCT CTT CAT TCA ATT GTC CAC GTT CAA TTA AGC AAC AGG G, and

GCT CTG CAT TCA AAC GTC CGC GTT CAA TAA AGA AAC AGG G;

and a nucleic acid sequence substantially complementary thereto.

250. A nucleotide polymer comprising a member of the group consisting of nucleotide polymers of the structures

CCC GAC CGT CCC TAT TAA TCA TTA CGA TGG,

CCCGACCGTCCCTATTAATCATTACGATGGTCCTAGAAAC

CCCGACCGTCCCTATTAATCATTACGATGG

CGA CTT GGC ATG AAA ACT ATT CCT TCC TAT GG,

GCT CTT CAT TCA ATT GTC CAC GTT CAA TTA AGC AAC AGG G, and

GCT CTG CAT TCA AAC GTC CGC GTT CAA TAA AGA AAC AGG G;

and the complements thereto.

251. A nucleotide polymer capable of hybridizing to the RNA of the phylogenetic group Fungi in the region corresponding to position 845-880 of Saccharomyces cerevisiae 18S rRNA.

252. A nucleic acid hybrid formed between a nucleotide polymer of claim 251 and a nucleic acid sequence substantially complementary thereto.

253. A nucleotide polymer capable of hybridizing to the RNA of the phylogenetic group Fungi in the region corresponding to position 1960-2000 of Saccharomyces cerevisiae

28S rRNA.

254. A nucleic acid hybrid formed between a nucleotide polymer of claim 253 and a nucleic acid substantially complementary thereto.

255. A nucleotide polymer capable of hybridizing to the RNA of the phylogenetic group Fungi in the region corresponding to position 1225-1270 of Saccharomyces cerevisiae 28S rRNA.

256. A nucleic acid hybrid formed between a nucleotide polymer of claim 255 and a nucleic acid substantially complementary thereto.

257. The probe of claim 31 wherein said non-viral organism is Neisseria gonorrhoeae.

258. The probe of claim 257 wherein said oligonucleotide comprises the sequence

CCG CCG CTA CCC GGT AC.

259. The probe of claim 257 wherein said oligonucleotide comprises the sequence

TCA TCG GCC GCC GAT ATT GGC.

260. The probe of claim 257 wherein said oligonucleotide comprises the sequence

GAG CAT TCC GCA CAT GTC AAA ACC AGG TA.

261. The probe of claim 257 wherein said oligonucleotide comprises the sequence

GAG GAT TCC GCA CAT GTC AAA ACC AGG.

262. The probe of claim 257 wherein said oligonucleotide comprises the sequence

GAG GAT TCC GCA CAT GTC AAA ACC AGG TAA.

263. The probe of claim 257 wherein said

oligonucleotide comprises the sequence

CCC GCT ACC CGG TAC GTTC.

264. The probe of claim 257 wherein said oligonucleotide comprises the sequence

CCG CTA CCC GGTAC GTTC.

265. A nucleotide polymer capable of hybridizing to the probes of claims 258 or 259 or 260 or 261 or 262 or 263 or 264 or to the complements thereof.

266. A nucleic acid hybrid formed between an oligonucleotide comprising a member of the group consisting of oligonucleotides of the sequences

CCGCCGCTACCCGGTAC,

TCATCGGCCGCCGATATTGGC,

GAGCATTCCGCACATGTCAAAACCAGGTA,

GAGGATTCCGCACATGTCAAAACCAGG,

GAGGATTCCGCACATGTCAAAACCAGGTAA,

CCCGCTACCCGGTACGTTC, and

CCGCTACCCGGTACGTTC;

and a nucleic acid sequence substantially complementary thereto.

267. A nucleotide polymer comprising a member of the group consisting of nucleotide polymers of the structures

CCGCCGCTACCCGGTAC,

TCATCGGCCGCCGATATTGGC,

GAGCATTCCGCACATGTCAAAACCAGGTA,

GAGGATTCCGCACATGTCAAAACCAGG,

GAGGATTCCGCACATGTCAAAACCAGGTAA,

CCCGCTACCCGGTACGTTC, and

CCGCTACCCGGTACGTTC;

and the complements thereto.

268. A nucleotide polymer capable of hybridizing to the RNA of the species Neisseria gonorrhoeae in the region corresponding to bases 125-150 of E. coli 16s rRNA.

269. A nucleic acid hybrid formed between a nucleotide polymer of claim 268 and a nucleic acid sequence substantially complementary thereto.

270. A nucleotide polymer capable of hybridizing to the RNA of the species Neisseria gonorrhoeae in the region corres-ponding to bases 455-485 of E. coli 16s rRNA.

271. A nucleic acid hybrid formed between a nucleotide polymer of claim 270 and a nucleic acid sequence substantially complementary thereto.

272. A nucleotide polymer capable of hybridizing to the RNA of the species Neisseria gonorrhoeae in the region corresponding to bases 980-1015 of E. coli 16s rRNA.

273. A nucleic acid hybrid formed between a nucleotide polymer of claim 272 and a nucleic acid sequence substantially complementary thereto.

274. The probe of claim 31 wherein said oligonucleotide is perfectly complementary to said region of rRNA.

275. The probe of claim 31 wherein said oligonucleotide is about 20 nucleotides to about 50 nucleotides in length.

276. The probe of claim 31 wherein said oligonucleotide is at least about 95% complementary to a region of rRNA.

277. A hybridization assay comprising (1) reacting together any rRNA from a sample to be assayed for a non-

viral organism or organisms and an oligonucleotide probe of at least about 10 nucleotides in length which is at least about 75% complementary to a variable region of rRNA selected to be unique to said non-viral organism or organisms, (2) under conditions such that hybridization between the oligonucleotide probe and any sufficiently complementary sample rRNA can occur, and (3) observing and/or measuring said hybridization.

278. The assay of claim 277 wherein said hybridization between the oligonucleotide probe and any target sample rRNA is from at least about 10% to about 100%.

279. The assay of claim 277 wherein said oligonucleotide probe is cDNA.

280. The assay of claim 277 wherein said conditions include a temperature from about 25°C below Tm to about 1°C below Tm.

281. The assay of claim 277 which further comprises the parallel assay of a positive homologous control, or a positive heterologous control, or both.

282. The assay of claim 277 which further comprises the parallel assay of a negative control.

283. The assay of claim 277 wherein said conditions include agents for increased rates of hybridization.

284. The assay of claim 277 wherein said conditions are such as to promote maximum hybridization between the oligonucleotide probe and any complementary sample rRNA and minimum cross-reactivity between the oligonucleotide probe and any non-complementary sample rRNA.

285. The assay of claim 277 wherein said oligonucleotide probe is labelled.

286. The assay of claim 285 wherein said oligonucleotide probe is labelled with an isotopic, non-isotopic or chemiluminescent label.

287. The assay of claim 277 which further comprises the release of rRNA from the cells of said non-viral organism or organisms prior to the reacting together step.

288. The assay of claim 277 wherein said non-viral organism or organisms are Mycobacterium avium, Mycobacterium intracellulare, the Mycobacterium tuberculosis-complex bacteria, Mycobacterium genus, Mycoplasma pneumoniae, Legionella, Salmonella, Chlamydia trachomatis, Campylobacter, Proteus mirabilis, Enterococcus, Enterobacter cloacae, E. coli, Pseudomonas group I, bacteria or fungi.

289. The assay of claim 277 wherein said labelled oligonucleotide probe is about 20 nucleotides to about 50 nucleotides in length.

290. The assay of claim 277 wherein said labelled oligonucleotide probe is at least about 95% complementary to said variable region of rRNA.

291. The assay of claim 277 further comprising the use of one or more additional oligonucleotide probes of at least about 10 nucleotides in length and which are at least about 75% complementary to one or more additional variable regions of rRNA selected to be unique to said non-viral organisms.

292. The assay of claim 277 further comprising the use of one or more additional probes which identify one or more additional non-viral organisms, thereby expanding the group of non-viral organisms to be assayed.

293. A method for preparing a probe or

combination of probes for use in a qualitative or quantitative hybridization assay which comprises constructing a nucleotide polymer that is sufficiently complementary to hybridize a region of DNA or rRNA selected to distinguish a target non-viral organism or group of non-viral organisms sought to be detected from at least one nontarget organism or group or nontarget organisms which may be present in a sample, said region of DNA or rRNA being selected by:

comparing one or more DNA or rRNA sequences of said non-viral organism or group of non-viral organisms sought to be detected with one or more DNA or rRNA sequences of said nontarget organisms or group of nontarget organisms;

aligning said DNA or rRNA sequences of said non-viral organism or group of non-viral organisms to homologies with said DNA or rRNA sequences of said nontarget organisms or group of organisms so as to identify regions of homology;

selecting said nucleotide polymer by substantially maximizing the homology of said probe oligonucleotide to the regions of said DNA or rRNA of said non-viral organism or non-viral group of organisms sought to be detected while substantially minimizing the homology of said nucleotide polymer to DNA or rRNA sequences of said nontarget organisms or group of organisms sought to be distinguished therefrom.

294. A method as in claim 293 wherein said nontarget organisms or group of organisms are close phylogenetic relatives of said target organisms or group of organisms.

295. The method of claim 292 wherein said nucleotide polymer is at least about 90% homologous to the regions of said DNA or rRNA of said non-viral organism or non-viral group of

organisms sought to be detected.

296. The method of claim 292 wherein said probe oligonucleotide is less than about 90% homologous to DNA or rRNA sequences of said closest phylogenetic relatives sought to be distinguished therefrom.

297. The method of claim 293 or 294 or 295 or 296 comprising the further step of verifying said probe non-cross reactivity by hybridizing said probe oligonucleotide to non-viral organisms or groups of non-viral organisms sought to be distinguished by said probe.

298. A method for preparing a probe for use in a qualitative or quantitative hybridization assay which comprises constructing an oligonucleotide that is sufficiently complementary to hybridize a region of DNA or rRNA selected to be unique to a non-viral organism or group of non-viral organisms sought to be detected, said region of DNA or rRNA being selected by:

comparing one or more DNA or rRNA sequences of said non-viral organism or group of non-viral organisms sought to be detected with one or more DNA or rRNA sequences of its closest phylogenetic relatives;

aligning said DNA or rRNA sequences of said non-viral organism or group of non-viral organisms to homologies with said DNA or rRNA sequences of said closest phylogenetic relatives, so as to reveal the interspecies hypervariable DNA or rRNA regions;

selecting said probe oligonucleotide in said interspecies hypervariable region by substantially maximizing the homology of said probe oligonucleotide to the regions of said DNA

or rRNA of said non-viral organism or non-viral group of organisms sought to be detected while substantially minimizing the homology of said probe oligonucleotide to DNA or rRNA sequences of said closest phylogenetic relatives sought to be distinguished therefrom.

299. The method of claim 298 wherein said probe oligonucleotide is at least about 90% homologous to the regions of said DNA or rRNA of said non-viral organism or non-viral group of organisms sought to be detected.

300. The method of claim 298 wherein said probe oligonucleotide is less than about 90% homologous to DNA or rRNA sequences of said closest phylogenetic relatives sought to be distinguished therefrom.

301. The method of claim 298 or 299 or 300 comprising the further step of verifying said probe non-cross reactivity by hybridizing said probe oligonucleotide to non-viral organisms or groups of non-viral organisms sought to be distringuished by said probe.

302. A probe consisting of a nucleotide polymer which is capable of hybridizing to 16S like rRNA of a nonviral organism or group of organisms in the region corresponding to bases 60-100 of E.Coli 16S rRNA.

303. A nucleic acid hybrid formed between a nucleotide polymer of claim 302 and a nucleic acid sequence substantially complementary thereto.

304. A probe consisting of a nucleotide polymer which is capable of hybridizing to 16S like rRNA of a nonviral organism or group of organisms in the region corresponding to bases 120-150 of E.Coli 16S rRNA.

305. A nucleic acid hybrid formed between a nucleotide polymer of claim 304 and a nucleic acid sequence substantially complementary thereto.

306. A probe consisting of a nucleotide polymer which is capable of hybridizing to 16S like rRNA of a nonviral organism or group of organisms in the region corresponding to bases 170-230 of E.Coli 16S rRNA.

307. A nucleic acid hybrid formed between a nucleotide polymer of claim 306 and a nucleic acid sequence substantially complementary thereto.

308. A probe consisting of a nucleotide polymer which is capable of hybridizing to 16S like rRNA of a nonviral organism or group of organisms in the region corresponding to bases 405-480 of E.Coli 16S rRNA.

309. A nucleic acid hybrid formed between a nucleotide polymer of claim 308 and a nucleic acid sequence substantially complementary thereto.

310. A probe consisting of a nucleotide polymer which is capable of hybridizing to 16S like rRNA of a nonviral organism or group of organisms in the region corresponding to bases 600-670 of E.Coli 16S rRNA.

311. A nucleic acid hybrid formed between a nucleotide polymer of claim 310 and a nucleic acid sequence substantially complementary thereto.

312. A probe consisting of a nucleotide polymer which is capable of hybridizing to 16S like rRNA of a nonviral organism or group of organisms in the region corresponding to bases 820-860 of E.Coli 16S rRNA.

313. A nucleic acid hybrid formed between a

nucleotide polymer of claim 312 and a nucleic acid sequence substantially complementary thereto.

314. A probe consisting of a nucleotide polymer which is capable of hybridizing to 16S like rRNA of a nonviral organism or group of organisms in the region corresponding to bases 980-1050 of E.Coli 16S rRNA.

315. A nucleic acid hybrid formed between a nucleotide polymer of claim 314 and a nucleic acid sequence substantially complementary thereto.

316. A probe consisting of a nucleotide polymer which is capable of hybridizing to 16S like rRNA of a nonviral organism or group of organisms in the region corresponding to bases 1250-1290 of E.Coli 16S rRNA.

317. A nucleic acid hybrid formed between a nucleotide polymer of claim 316 and a nucleic acid sequence substantially complementary thereto.

318. A probe consisting of a nucleotide polymer which is capable of hybridizing to 23S like rRNA of a nonviral organism or group of organisms in the region corresponding to bases 270-390 of E.Coli 23S rRNA.

319. A nucleic acid hybrid formed between a nucleotide polymer of claim 318 and a nucleic acid sequence substantially complementary thereto.

320. A probe consisting of a nucleotide polymer which is capable of hybridizing to 23S like rRNA of a nonviral organism or group of organisms in the region corresponding to bases 535-560 of E.Coli 23S rRNA.

321. A nucleic acid hybrid formed between a nucleotide polymer of claim 320 and a nucleic acid sequence

substantially complementary thereto.

322. A probe consisting of a nucleotide polymer which is capable of hybridizing to 23S like rRNA of a nonviral organism or group of organisms in the region corresponding to bases 1150-1200 of E.Coli 23S rRNA.

323. A nucleic acid hybrid formed between a nucleotide polymer of claim 322 and a nucleic acid sequence substantially complementary thereto.

324. A probe consisting of a nucleotide polymer which is capable of hybridizing to 23S like rRNA of a nonviral organism or group of organisms in the region corresponding to bases 1440-1600 of E.Coli 23S rRNA.

325. A nucleic acid hybrid formed between a nucleotide polymer of claim 324 and a nucleic acid sequence substantially complementary thereto.

326. A probe consisting of a nucleotide polymer which is capable of hybridizing to 23S like rRNA of a nonviral organism or group of organisms in the region corresponding to bases 1710-1750 of E.Coli 23S rRNA.

327. A nucleic acid hybrid formed between a nucleotide polymer of claim 326 and a nucleic acid sequence substantially complementary thereto.

328. A probe consisting of a nucleotide polymer which is capable of hybridizing to 23S like rRNA of a nonviral organism or group of organisms in the region corresponding to bases 2190-2330 of E.Coli 23S rRNA.

329. A nucleic acid hybrid formed between a nucleotide polymer of claim 328 and a nucleic acid sequence substantially complementary thereto.